

SEQUENCE LISTING

<110> Oy Jurilab Ltd

<120> Method for detecting the risk of acute myocardial infarction and coronary heart disease

<130> 40597

<160> 56

<170> PatentIn version 3.1

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cacattgcca aacacgat 18

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caggctgact cctcactccc cacatatcca ctctgctct cctcctgca ggtgacccca 180
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<222> (1)..(1344)

<223> Coding sequence for variant human ADRA2B gene

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Met	Asp	His	Gln	Asp	Pro	Tyr	Ser	Val	Gln	Ala	Thr	Ala	Ala	Ile	Ala	
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gcg	gcc	atc	acc	ttc	ctc	att	ctc	ttt	acc	atc	ttc	ggc	aac	gct	ctg	96
Ala	Ala	Ile	Thr	Phe	Leu	Ile	Leu	Phe	Thr	Ile	Phe	Gly	Asn	Ala	Leu	
			20					25					30			

gtc	atc	ctg	gct	gtg	ttg	acc	agc	cgc	tcg	ctg	cgc	gcc	cct	cag	aac	144
Val	Ile	Leu	Ala	Val	Leu	Thr	Ser	Arg	Ser	Leu	Arg	Ala	Pro	Gln	Asn	
		35				40						45				

ctg	ttc	ctg	gtg	tcg	ctg	gcc	gcc	gcc	gac	atc	ctg	gtg	gcc	acg	ctc	192
Leu	Phe	Leu	Val	Ser	Leu	Ala	Ala	Ala	Asp	Ile	Leu	Val	Ala	Thr	Leu	
	50					55					60					

atc	atc	cct	ttc	tcg	ctg	gcc	aac	gag	ctg	ctg	ggc	tac	tgg	tac	ttc	240
Ile	Ile	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Leu	Leu	Gly	Tyr	Trp	Tyr	Phe	
65					70				75						80	

cgg	cgc	acg	tgg	tgc	gag	gtg	tac	ctg	gcg	ctc	gac	gtg	ctc	ttc	tgc	288
Arg	Arg	Thr	Trp	Cys	Glu	Val	Tyr	Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	
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acc	tcg	tcc	atc	gtg	cac	ctg	tgc	gcc	atc	agc	ctg	gac	cgc	tac	tgg	336
Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	
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gcc	gtg	agc	cgc	gcg	ctg	gag	tac	aac	tcc	aag	cgc	acc	ccg	cgc	cgc	384
Ala	Val	Ser	Arg	Ala	Leu	Glu	Tyr	Asn	Ser	Lys	Arg	Thr	Pro	Arg	Arg	
		115				120						125				

atc	aag	tgc	atc	atc	ctc	act	gtg	tgg	ctc	atc	gcc	gcc	gtc	atc	tcg	432
Ile	Lys	Cys	Ile	Ile	Leu	Thr	Val	Trp	Leu	Ile	Ala	Ala	Val	Ile	Ser	
	130					135					140					

ctg	ccg	ccc	ctc	atc	tac	aag	ggc	gac	cag	ggc	ccc	cag	ccg	cgc	ggg	480
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Leu 145	Pro	Pro	Leu	Ile	Tyr 150	Lys	Gly	Asp	Gln	Gly 155	Pro	Gln	Pro	Arg	Gly 160	
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Arg	Pro	Gln	Cys	Lys 165	Leu	Asn	Gln	Glu	Ala 170	Trp	Tyr	Ile	Leu	Ala 175	Ser	
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Ser	Ile	Gly	Ser 180	Phe	Phe	Ala	Pro	Cys 185	Leu	Ile	Met	Ile	Leu 190	Val	Tyr	
ctg	cgc	atc	tac	ctg	atc	gcc	aaa	cgc	agc	aac	cgc	aga	ggc	ccc	agg	624
Leu	Arg	Ile 195	Tyr	Leu	Ile	Ala	Lys 200	Arg	Ser	Asn	Arg	Arg 205	Gly	Pro	Arg	
gcc	aag	ggg	ggg	cct	ggg	cag	ggc	gag	tcc	aag	cag	ccc	cga	ccc	gac	672
Ala	Lys 210	Gly	Gly	Pro	Gly	Gln 215	Gly	Glu	Ser	Lys	Gln 220	Pro	Arg	Pro	Asp	
cat	ggc	ggg	gct	ttg	gcc	tca	gcc	aaa	ctg	cca	gcc	ctg	gcc	tct	gtg	720
His 225	Gly	Gly	Ala	Leu	Ala 230	Ser	Ala	Lys	Leu 235	Pro	Ala	Leu	Ala	Ser	Val 240	
gct	tct	gcc	aga	gag	gtc	aac	gga	cac	tcg	aag	tcc	act	ggg	gag	aag	768
Ala	Ser	Ala	Arg 245	Glu	Val	Asn	Gly	His	Ser 250	Lys	Ser	Thr	Gly	Glu 255	Lys	
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Glu	Glu	Gly	Glu 260	Thr	Pro	Glu	Asp	Thr 265	Gly	Thr	Arg	Ala	Leu 270	Pro	Pro	
agt	tgg	gct	gcc	ctt	ccc	aac	tca	ggc	cag	ggc	cag	aag	gag	ggc	gtt	864
Ser	Trp 275	Ala	Ala	Leu	Pro	Asn	Ser 280	Gly	Gln	Gly	Gln	Lys 285	Glu	Gly	Val	
tgt	ggg	gca	tct	cca	gag	gat	gaa	gct	gaa	gag	gag	gaa	gag	gag	gag	912
Cys	Gly 290	Ala	Ser	Pro	Glu	Asp 295	Glu	Ala	Glu	Glu	Glu 300	Glu	Glu	Glu	Glu	
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Glu	Glu	Cys	Glu	Pro	Gln 310	Ala	Val	Pro	Val	Ser 315	Pro	Ala	Ser	Ala	Cys 320	
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Ser	Pro	Pro	Leu 325	Gln	Gln	Pro	Gln	Gly	Ser 330	Arg	Val	Leu	Ala 335	Thr	Leu	
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Arg	Gly	Gln 340	Val	Leu	Leu	Gly	Arg	Gly 345	Val	Gly	Ala	Ile	Gly 350	Gly	Gln	
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Trp	Trp	Arg 355	Arg	Arg	Ala	His	Val 360	Thr	Arg	Glu	Lys	Arg 365	Phe	Thr	Phe	
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Val	Leu 370	Ala	Val	Val	Ile	Gly 375	Val	Phe	Val	Leu	Cys 380	Trp	Phe	Pro	Phe	
ttc	ttc	agc	tac	agc	ctg	ggc	gcc	atc	tgc	ccg	aag	cac	tgc	aag	gtg	1200
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Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser							
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tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt							1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg							
		420		425		430	
gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga							1344
Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp							
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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175
 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
 180 185 190
 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
 195 200 205
 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
 210 215 220
 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240
 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255
 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270
 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285
 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
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 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
 305 310 315 320
 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
 325 330 335
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
 340 345 350
 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
 355 360 365
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
 370 375 380
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
 385 390 395 400
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser

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Ser	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Ile	Phe	Asn	Gln	Asp	Phe	Arg	Arg
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gcg	gcc	atc	acc	ttc	ctc	att	ctc	ttt	acc	atc	ttc	ggc	aac	gct	ctg	96
Ala	Ala	Ile	Thr	Phe	Leu	Ile	Leu	Phe	Thr	Ile	Phe	Gly	Asn	Ala	Leu	
			20					25					30			
gtc	atc	ctg	gct	gtg	ttg	acc	agc	cgc	tcg	ctg	cgc	gcc	cct	cag	aac	144
Val	Ile	Leu	Ala	Val	Leu	Thr	Ser	Arg	Ser	Leu	Arg	Ala	Pro	Gln	Asn	
		35				40						45				
ctg	ttc	ctg	gtg	tcg	ctg	gcc	gcc	gcc	gac	atc	ctg	gtg	gcc	acg	ctc	192
Leu	Phe	Leu	Val	Ser	Leu	Ala	Ala	Ala	Asp	Ile	Leu	Val	Ala	Thr	Leu	
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atc	atc	cct	ttc	tcg	ctg	gcc	aac	gag	ctg	ctg	ggc	tac	tgg	tac	ttc	240
Ile	Ile	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Leu	Leu	Gly	Tyr	Trp	Tyr	Phe	
65					70				75						80	
cgg	cgc	acg	tgg	tgc	gag	gtg	tac	ctg	gcg	ctc	gac	gtg	ctc	ttc	tgc	288
Arg	Arg	Thr	Trp	Cys	Glu	Val	Tyr	Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	
				85					90					95		
acc	tcg	tcc	atc	gtg	cac	ctg	tgc	gcc	atc	agc	ctg	gac	cgc	tac	tgg	336
Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	
			100					105					110			
gcc	gtg	agc	cgc	gcg	ctg	gag	tac	aac	tcc	aag	cgc	acc	ccg	cgc	cgc	384
Ala	Val	Ser	Arg	Ala	Leu	Glu	Tyr	Asn	Ser	Lys	Arg	Thr	Pro	Arg	Arg	
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Ile	Lys	Cys	Ile	Ile	Leu	Thr	Val	Trp	Leu	Ile	Ala	Ala	Val	Ile	Ser	
	130					135					140					
ctg	ccg	ccc	ctc	atc	tac	aag	ggc	gac	cag	ggc	ccc	cag	ccg	cgc	ggg	480
Leu	Pro	Pro	Leu	Ile	Tyr	Lys	Gly	Asp	Gln	Gly	Pro	Gln	Pro	Arg	Gly	
145					150					155					160	

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Arg	Pro	Gln	Cys	Lys	Leu	Asn	Gln	Glu	Ala	Trp	Tyr	Ile	Leu	Ala	Ser	
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agc	atc	gga	tct	ttc	ttt	gct	cct	tgc	ctc	atc	atg	atc	ctt	gtc	tac	576
Ser	Ile	Gly	Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr	
			180					185					190			
ctg	cgc	atc	tac	ctg	atc	gcc	aaa	cgc	agc	aac	cgc	aga	ggc	ccc	agg	624
Leu	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Arg	Ser	Asn	Arg	Arg	Gly	Pro	Arg	
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gcc	aag	ggg	ggg	cct	ggg	cag	ggc	gag	tcc	aag	cag	ccc	cga	ccc	gac	672
Ala	Lys	Gly	Gly	Pro	Gly	Gln	Gly	Glu	Ser	Lys	Gln	Pro	Arg	Pro	Asp	
	210					215					220					
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His	Gly	Gly	Ala	Leu	Ala	Ser	Ala	Lys	Leu	Pro	Ala	Leu	Ala	Ser	Val	
225					230					235					240	
gct	tct	gcc	aga	gag	gtc	aac	gga	cac	tgc	aag	tcc	act	ggg	gag	aag	768
Ala	Ser	Ala	Arg	Glu	Val	Asn	Gly	His	Ser	Lys	Ser	Thr	Gly	Glu	Lys	
				245					250					255		
gag	gag	ggg	gag	acc	cct	gaa	gat	act	ggg	acc	cgg	gcc	ttg	cca	ccc	816
Glu	Glu	Gly	Glu	Thr	Pro	Glu	Asp	Thr	Gly	Thr	Arg	Ala	Leu	Pro	Pro	
			260					265					270			
agt	tgg	gct	gcc	ctt	ccc	aac	tca	ggc	cag	ggc	cag	aag	gag	ggc	gtt	864
Ser	Trp	Ala	Ala	Leu	Pro	Asn	Ser	Gly	Gln	Gly	Gln	Lys	Glu	Gly	Val	
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Cys	Gly	Ala	Ser	Pro	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
	290					295					300					
gag	gag	gag	gaa	gag	tgt	gaa	ccc	cag	gca	gtg	cca	gtg	tct	ccg	gcc	960
Glu	Glu	Glu	Glu	Glu	Cys	Glu	Pro	Gln	Ala	Val	Pro	Val	Ser	Pro	Ala	
305					310					315					320	
tca	gct	tgc	agc	ccc	ccg	ctg	cag	cag	cca	cag	ggc	tcc	cgg	gtg	ctg	1008
Ser	Ala	Cys	Ser	Pro	Pro	Leu	Gln	Gln	Pro	Gln	Gly	Ser	Arg	Val	Leu	
				325					330					335		
gcc	acc	cta	cgt	ggc	cag	gtg	ctc	ctg	ggc	agg	ggc	gtg	ggc	gct	ata	1056
Ala	Thr	Leu	Arg	Gly	Gln	Val	Leu	Leu	Gly	Arg	Gly	Val	Gly	Ala	Ile	
			340					345					350			
ggc	ggg	cag	tgg	tgg	cgt	cga	agg	gcg	cac	gtg	acc	cgg	gag	aag	cgc	1104
Gly	Gly	Gln	Trp	Trp	Arg	Arg	Arg	Ala	His	Val	Thr	Arg	Glu	Lys	Arg	
		355					360					365				
ttc	acc	ttc	gtg	ctg	gct	gtg	gtc	att	ggc	gtt	ttt	gtg	ctc	tgc	tgg	1152
Phe	Thr	Phe	Val	Leu	Ala	Val	Val	Ile	Gly	Val	Phe	Val	Leu	Cys	Trp	
	370					375					380					
ttc	ccc	ttc	ttc	ttc	agc	tac	agc	ctg	ggc	gcc	atc	tgc	ccg	aag	cac	1200
Phe	Pro	Phe	Phe	Phe	Ser	Tyr	Ser	Leu	Gly	Ala	Ile	Cys	Pro	Lys	His	
385					390					395					400	

tgc aag gtg ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac 1248
 Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415

tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac 1296
 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
 420 425 430

ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg 1344
 Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
 435 440 445

gcc tgg tga 1353
 Ala Trp
 450

<210> 23
 <211> 450
 <212> PRT
 <213> Homo sapiens
 <400> 23

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160
 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175
 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
 180 185 190
 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
 195 200 205
 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
 210 215 220
 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240
 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255
 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270
 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285
 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300
 Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
 305 310 315 320
 Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
 325 330 335
 Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350
 Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
 355 360 365
 Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380
 Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His

385 390 395 400

Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
405 410 415

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
420 425 430

Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
435 440 445

Ala Trp
450

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<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 24
gggtgtttgt ggggcatctc
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20

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<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Snapshot primer
<400> 25
tggcactgcc tgggggttca
```

19

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<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Sequencing primer
<400> 26
tcagggtcttc tcccagca
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18

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<210> 27
<211> 619
<212> DNA
<213> Homo sapiens
<400> 27
ggatgaagca gaatgaagag taggtaaccc tgaggttgag aggtatattg ttggaccagg 60
gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120
tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
atcctaacat gactgataca gtgtctctta tttagactat ctcagttagt ctggctgtgc 240
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ttgtcctttt tcccacctcc ctgctgtgc ctgacctct cttctttcca caggttctca 300
ggcaagagcc acctgctatt gccgaaccgg ccgttgtgct acccgtgagt ccctctccgg 360
ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480
gtaccttggtg tctttctaaa tttctctctc caaagtaaag ttcaagcatt aaacttagtg 540
tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
tggtttgtat gggttccttt 619

```

```

<210> 28
<211> 619
<212> DNA
<213> Homo sapiens
<400> 28

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ggatgaagca gaatgaagag taggtaaccc tgaggttgag aggtatattg ttggaccagg 60
gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120
tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
atcctaacat gactgataca gtgtctctta tttagactat ctcaagttagt ctggctgtgc 240
ttgtcctttt tcccacctcc ctgctgtgc ctgacctct cttctttcca caggttctca 300
ggcaagagcc acctgctatt gccgaaccgg ccgttgtgct acccgtgagt ccctctccgg 360
ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480
gtaccttggtg tctttctaaa tttctctctc caaaataaag ttcaagcatt aaacttagtg 540
tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
tggtttgtat gggttccttt 619

```

```

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 29
ggatgaagca gaatgaaga 19

```

```

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 30

```

aaaggaacca tacaaccca

19

<210> 31

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequencing primer

<400> 31

gttagtctgg ctgtgctt

18

<210> 32

<211> 1052

<212> DNA

<213> Homo sapiens

<400> 32

gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60

cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120

ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180

catcctaaaa gcaaataatt actctatcat ctacgtgccc ttgcttctt aaagttactc 240

aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300

cagcctgccc atttgccttc atcaacattc ctaaacactg ggcttaaaat gtagtatgag 360

taaactctct cttagtctat ccctctccca ctagcagttt taacatcatc tctagttatt 420

aaccttggct caatggcttt ctctcttttt ttatacaga atttattggc ttgagacgct 480

gtttaatggg ttgggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga 540

aatgcaagat gaaaaaatgt tgtgttggac caaaagtggg taaattgatt aaaaactacc 600

tgcaatatgg aacaccaa atgtacttaatg aagacgtcca agaaatgcta aaacctgcca 660

agaattctag tgctgtgata caaagaaaac atattttatc tgttctcccc caaatcaaaa 720

gcactagctt ttttgcta atccaactttg tcatcattcc aaatgccacc cctatgaact 780

ctgccaccat cagcactatg accccaggac agatcacata cactgctact tctaccaaga 840

gtaacaccaa agaaagcaga gattctgcca ctgcctcgcc accaccagca ccacctccac 900

caaacatact gccaacacca tcaactggagc tagaggaagc agaagagcag taatgtggat 960

ctttccctta aaactccaag ttctctctta tttttgctat ctataaaatg acatagaact 1020

gtttcctctg tcatcagtc ttcaataaac ac 1052

<210> 33

<211> 1049

<212> DNA

<213> Homo sapiens

<400> 33


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gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa      60
cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat      120
ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc      180
catcctaaaa gcaaataatt actctatcat ctacgtgccc ttgcttctt aaagttactc      240
aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct      300
cagcctgccc atttgccttc atcaacattc ctaaacactg ggcttaaaat gtagtatgag      360
taaactctct cttagtctat ccactctcca ctagcagttt taacatcatc tctagttatt      420
aaccttggct caatggcttt ctcttttttt atacagaatt tattggcttg agacgctggt      480
taatgggttt ggggagatgc agggatcact gcaatgtgga tgaaaaagag atacagaaat      540
gcaagatgaa aaaatgttgt gttggaccaa aagtgggtta attgattaaa aactacctgc      600
aatatggaac accaaatgta cttaatgaag acgtccaaga aatgctaaaa cctgccaaga      660
attctagtgc tgtgatacaa agaaaacata ttttatctgt tctcccccaa atcaaaagca      720
ctagcttttt tgctaatacc aactttgtca tcattccaaa tgccaccctt atgaactctg      780
ccaccatcag cactatgacc ccaggacaga tcacatacac tgctacttct accaagagta      840
acaccaaaga aagcagagat tctgccactg cctcgccacc accagcacca cctccaccaa      900
acatactgcc aacaccatca ctggagctag aggaagcaga agagcagtaa tgtggatctt      960
tcccttaaaa ctccaagttc ctctctattt ttgctatcta taaaatgaca tagaactggt      1020
tcctctgtca tcagtcattc aataaacac                                     1049

```

```

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 34
ggctactgag tttggtga

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18

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<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 35
gtgtttattg aatgactgat g

```

21

```

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

```


<220>
 <223> Sequencing primer
 <400> 36
 caaggaaggc agactaaa 18

<210> 37
 <211> 552
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the variant human DEFB129 gene
 <400> 37

atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432
 Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
 130 135 140

acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca 480
 Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag 528
 Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

cta gag gaa gca gaa gag cag taa 552
 Leu Glu Glu Ala Glu Glu Gln

180

<210> 38
 <211> 183
 <212> PRT
 <213> Homo sapiens
 <400> 38

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
 130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 39
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(552)

<223> Coding sequence for the human DEFB129 gene

<400> 39

atg	aag	ctc	ctt	ttt	cct	atc	ttt	gcc	agc	ctc	atg	cta	cag	tac	cag	48
Met	Lys	Leu	Leu	Phe	Pro	Ile	Phe	Ala	Ser	Leu	Met	Leu	Gln	Tyr	Gln	
1				5				10					15			

gtg	aac	aca	gaa	ttt	att	ggc	ttg	aga	cgc	tgt	tta	atg	ggg	ttg	ggg	96
Val	Asn	Thr	Glu	Phe	Ile	Gly	Leu	Arg	Arg	Cys	Leu	Met	Gly	Leu	Gly	
			20					25					30			

aga	tgc	agg	gat	cac	tgc	aat	gtg	gat	gaa	aaa	gag	ata	cag	aaa	tgc	144
Arg	Cys	Arg	Asp	His	Cys	Asn	Val	Asp	Glu	Lys	Glu	Ile	Gln	Lys	Cys	
		35					40					45				

aag	atg	aaa	aaa	tgt	tgt	ggt	gga	cca	aaa	gtg	ggt	aaa	ttg	att	aaa	192
Lys	Met	Lys	Lys	Cys	Cys	Val	Gly	Pro	Lys	Val	Val	Lys	Leu	Ile	Lys	
	50					55					60					

aac	tac	cta	caa	tat	gga	aca	cca	aat	gta	ctt	aat	gaa	gac	gtc	caa	240
Asn	Tyr	Leu	Gln	Tyr	Gly	Thr	Pro	Asn	Val	Leu	Asn	Glu	Asp	Val	Gln	
65					70					75					80	

gaa	atg	cta	aaa	cct	gcc	aag	aat	tct	agt	gct	gtg	ata	caa	aga	aaa	288
Glu	Met	Leu	Lys	Pro	Ala	Lys	Asn	Ser	Ser	Ala	Val	Ile	Gln	Arg	Lys	
				85				90						95		

cat	att	tta	tct	gtt	ctc	ccc	caa	atc	aaa	agc	act	agc	ttt	ttt	gct	336
His	Ile	Leu	Ser	Val	Leu	Pro	Gln	Ile	Lys	Ser	Thr	Ser	Phe	Phe	Ala	
			100					105					110			

aat	acc	aac	ttt	gtc	atc	att	cca	aat	gcc	acc	cct	atg	aac	tct	gcc	384
Asn	Thr	Asn	Phe	Val	Ile	Ile	Pro	Asn	Ala	Thr	Pro	Met	Asn	Ser	Ala	
		115					120					125				

acc	atc	agc	act	atg	acc	cca	gga	cag	atc	aca	tac	act	gct	act	tct	432
Thr	Ile	Ser	Thr	Met	Thr	Pro	Gly	Gln	Ile	Thr	Tyr	Thr	Ala	Thr	Ser	
		130				135					140					

acc	aag	agt	aac	acc	aaa	gaa	agc	aga	gat	tct	gcc	act	gcc	tcg	cca	480
Thr	Lys	Ser	Asn	Thr	Lys	Glu	Ser	Arg	Asp	Ser	Ala	Thr	Ala	Ser	Pro	
145					150					155					160	

cca	cca	gca	cca	cct	cca	cca	aac	ata	ctg	cca	aca	cca	tca	ctg	gag	528
Pro	Pro	Ala	Pro	Pro	Pro	Pro	Asn	Ile	Leu	Pro	Thr	Pro	Ser	Leu	Glu	
				165					170					175		

cta	gag	gaa	gca	gaa	gag	cag	taa									552
Leu	Glu	Glu	Ala	Glu	Glu	Gln										
			180													

<210> 40

<211> 183

<212> PRT

<213> Homo sapiens

<400> 40

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln

1				5				10				15			
Val	Asn	Thr	Glu 20	Phe	Ile	Gly	Leu	Arg 25	Arg	Cys	Leu	Met	Gly 30	Leu	Gly
Arg	Cys	Arg 35	Asp	His	Cys	Asn	Val 40	Asp	Glu	Lys	Glu	Ile 45	Gln	Lys	Cys
Lys	Met 50	Lys	Lys	Cys	Cys	Val 55	Gly	Pro	Lys	Val	Val 60	Lys	Leu	Ile	Lys
Asn 65	Tyr	Leu	Gln	Tyr	Gly 70	Thr	Pro	Asn	Val	Leu 75	Asn	Glu	Asp	Val	Gln 80
Glu	Met	Leu	Lys	Pro 85	Ala	Lys	Asn	Ser	Ser 90	Ala	Val	Ile	Gln	Arg 95	Lys
His	Ile	Leu	Ser 100	Val	Leu	Pro	Gln	Ile 105	Lys	Ser	Thr	Ser	Phe 110	Phe	Ala
Asn	Thr	Asn 115	Phe	Val	Ile	Ile	Pro 120	Asn	Ala	Thr	Pro	Met 125	Asn	Ser	Ala
Thr	Ile 130	Ser	Thr	Met	Thr	Pro 135	Gly	Gln	Ile	Thr	Tyr 140	Thr	Ala	Thr	Ser
Thr 145	Lys	Ser	Asn	Thr	Lys 150	Glu	Ser	Arg	Asp	Ser 155	Ala	Thr	Ala	Ser	Pro 160
Pro	Pro	Ala	Pro	Pro 165	Pro	Pro	Asn	Ile	Leu 170	Pro	Thr	Pro	Ser	Leu 175	Glu
Leu	Glu	Glu	Ala 180	Glu	Glu	Gln									

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<210> 41
<211> 372
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(372)
<223> Coding sequence for the variant human DEFB118 gene
<400> 41
atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1 5 10 15
gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96

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21

Val	Ile	Pro	Ala	Tyr	Ser	Gly	Glu	Lys	Lys	Cys	Trp	Asn	Arg	Ser	Gly		
			20					25					30				
cac	cgc	agg	aaa	caa	tgc	aaa	gat	gga	gaa	gca	gtg	aaa	gat	aca	tgc		144
His	Arg	Arg	Lys	Gln	Cys	Lys	Asp	Gly	Glu	Ala	Val	Lys	Asp	Thr	Cys		
		35					40					45					
aaa	aat	ctt	cga	gct	tgc	tgc	att	cca	tcc	aat	gaa	gac	cac	agg	cga		192
Lys	Asn	Leu	Arg	Ala	Cys	Cys	Ile	Pro	Ser	Asn	Glu	Asp	His	Arg	Arg		
	50					55					60						
gtt	cct	gcg	aca	tct	ccc	aca	ccc	ttg	agt	gac	tca	aca	cca	gga	att		240
Val	Pro	Ala	Thr	Ser	Pro	Thr	Pro	Leu	Ser	Asp	Ser	Thr	Pro	Gly	Ile		
65					70					75					80		
att	gat	gat	att	tta	aca	gta	agg	ttc	acg	aca	gac	tac	ttt	gaa	gta		288
Ile	Asp	Asp	Ile	Leu	Thr	Val	Arg	Phe	Thr	Thr	Asp	Tyr	Phe	Glu	Val		
				85					90					95			
agc	agc	aag	aaa	gat	atg	gtt	gaa	gag	tct	gag	gcg	gga	agg	gga	act		336
Ser	Ser	Lys	Lys	Asp	Met	Val	Glu	Glu	Ser	Glu	Ala	Gly	Arg	Gly	Thr		
			100					105					110				
gag	acc	tct	ctt	cca	aat	gtt	cac	cat	agc	tca	tga						372
Glu	Thr	Ser	Leu	Pro	Asn	Val	His	His	Ser	Ser							
		115					120										

<210> 42
 <211> 123
 <212> PRT
 <213> Homo sapiens
 <400> 42

Met	Lys	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Met	Leu	Val	Leu	Leu	Pro	Gln		
1				5				10						15			
Val	Ile	Pro	Ala	Tyr	Ser	Gly	Glu	Lys	Lys	Cys	Trp	Asn	Arg	Ser	Gly		
			20					25					30				
His	Arg	Arg	Lys	Gln	Cys	Lys	Asp	Gly	Glu	Ala	Val	Lys	Asp	Thr	Cys		
		35					40					45					
Lys	Asn	Leu	Arg	Ala	Cys	Cys	Ile	Pro	Ser	Asn	Glu	Asp	His	Arg	Arg		
	50					55					60						
Val	Pro	Ala	Thr	Ser	Pro	Thr	Pro	Leu	Ser	Asp	Ser	Thr	Pro	Gly	Ile		
65					70					75					80		
Ile	Asp	Asp	Ile	Leu	Thr	Val	Arg	Phe	Thr	Thr	Asp	Tyr	Phe	Glu	Val		
				85					90					95			
Ser	Ser	Lys	Lys	Asp	Met	Val	Glu	Glu	Ser	Glu	Ala	Gly	Arg	Gly	Thr		
			100					105					110				

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 43
 <211> 372
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence of the human DEFB118 gene

<400> 43
 atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15
 gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30
 cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc 144
 His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45
 aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga 192
 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60
 gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att 240
 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80
 att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta 288
 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95
 agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act 336
 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110
 gag acc tct ctt cca aat gtt cac cat agc tca tga 372
 Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 44
 <211> 123
 <212> PRT
 <213> Homo sapiens
 <400> 44

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 45
 aggttgagta tttgccagac

20

<210> 46
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 46
 aggacagggg tgagtgata

19

<210> 47
 <211> 246
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(246)
 <223> Coding sequence for the variant human DEFB126 gene
 <400> 47

atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa
 Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1 5 10 15

48

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga
 Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
 20 25 30

96

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt	144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	
tgg gca atg tgc ggc aaa ggg act gct gtg ttc cag ctg aca gac gtg	192
Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val	
50 55 60	
cta att atc ctg ttt tct gtg tcc aga caa aga cta caa gaa ttt caa	240
Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln	
65 70 75 80	
cag taa	246
Gln	

<210> 48
 <211> 81
 <212> PRT
 <213> Homo sapiens
 <400> 48

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
50 55 60

Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
65 70 75 80

Gln

<210> 49
 <211> 336
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(336)
 <223> Coding sequence of the human DEFB126 gene
 <400> 49

atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa	48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln	
1 5 10 15	

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga	96
---	----

Leu	Val	Ser	Gly	Asn	Trp	Tyr	Val	Lys	Lys	Cys	Leu	Asn	Asp	Val	Gly		
			20					25					30				
att	tgc	aag	aag	aag	tgc	aaa	cct	gaa	gag	atg	cat	gta	aag	aat	ggt		144
Ile	Cys	Lys	Lys	Lys	Cys	Lys	Pro	Glu	Glu	Met	His	Val	Lys	Asn	Gly		
		35					40					45					
tgg	gca	atg	tgc	ggc	aaa	caa	agg	gac	tgc	tgt	gtt	cca	gct	gac	aga		192
Trp	Ala	Met	Cys	Gly	Lys	Gln	Arg	Asp	Cys	Cys	Val	Pro	Ala	Asp	Arg		
	50					55					60						
cgt	gct	aat	tat	cct	gtt	ttc	tgt	gtc	cag	aca	aag	act	aca	aga	att		240
Arg	Ala	Asn	Tyr	Pro	Val	Phe	Cys	Val	Gln	Thr	Lys	Thr	Thr	Arg	Ile		
65					70				75						80		
tca	aca	gta	aca	gca	aca	aca	gca	aca	aca	act	ttg	atg	atg	act	act		288
Ser	Thr	Val	Thr	Ala	Thr	Thr	Ala	Thr	Thr	Thr	Leu	Met	Met	Thr	Thr		
				85				90						95			
gct	tcg	atg	tct	tcg	atg	gct	cct	acc	ccc	gtt	tct	ccc	act	ggt	tga		336
Ala	Ser	Met	Ser	Ser	Met	Ala	Pro	Thr	Pro	Val	Ser	Pro	Thr	Gly			
			100				105						110				

<210> 50
 <211> 111
 <212> PRT
 <213> Homo sapiens
 <400> 50

Met	Lys	Ser	Leu	Leu	Phe	Thr	Leu	Ala	Val	Phe	Met	Leu	Leu	Ala	Gln		
1			5						10					15			

Leu	Val	Ser	Gly	Asn	Trp	Tyr	Val	Lys	Lys	Cys	Leu	Asn	Asp	Val	Gly		
			20					25					30				

Ile	Cys	Lys	Lys	Lys	Cys	Lys	Pro	Glu	Glu	Met	His	Val	Lys	Asn	Gly		
		35					40					45					

Trp	Ala	Met	Cys	Gly	Lys	Gln	Arg	Asp	Cys	Cys	Val	Pro	Ala	Asp	Arg		
	50					55					60						

Arg	Ala	Asn	Tyr	Pro	Val	Phe	Cys	Val	Gln	Thr	Lys	Thr	Thr	Arg	Ile		
65					70				75						80		

Ser	Thr	Val	Thr	Ala	Thr	Thr	Ala	Thr	Thr	Thr	Leu	Met	Met	Thr	Thr		
				85				90						95			

Ala	Ser	Met	Ser	Ser	Met	Ala	Pro	Thr	Pro	Val	Ser	Pro	Thr	Gly			
			100					105					110				

<210> 51
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

aatggtgaga aagatgacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

gttgaatgga gggaaagt

18

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequencing primer

<400> 53

gtaggtatatt atgattag

18

<210> 54

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(333)

<223> Coding sequence for the variant human DEFB126 gene

<400> 54

atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

48

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

96

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

144

tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
50 55 60

192

cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65 70 75 80

240

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
85 90 95

288

gct tcg atg tct tcg atg gct cct acc cgt ttc tcc cac tgg ttg a

334

27

Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu
100 105 110

<210> 55
<211> 111
<212> PRT
<213> Homo sapiens
<400> 55

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
50 55 60

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65 70 75 80

Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
85 90 95

Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu
100 105 110

<210> 56
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> snapshot primer
<400> 56

tttttttttt tttttttttt tttttttttt ttgtctcaat ggctttctct

50